ABSTRACT

The invention provides methods and devices for analyzing sequence variations in nucleic acid samples comprising multiple loci, each having two, three or more possible allelic sequences. The method involves combining at least a first and second pair of oligonucleotide probes with the nucleic acid sample. The first pair of probes is capable of hybridizing in proximity to each other within a segment of the nucleic acid sample comprising the first locus and the second pair is capable of hybridizing in proximity to each other within a segment of the nucleic acid sample comprising the second locus. The first member of each probe pair comprises a FRET donor and the second member comprises a FRET acceptor, the FRET acceptor of the first probe pair member having a different emission spectrum from the FRET acceptor of the second probe pair. Upon hybridization, the proximity of the first and second member of each probe pair is sufficient to allow fluorescence resonance energy transfer between the FRET donor and the FRET acceptor.